

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/725,188A  
Source: IFW/6  
Date Processed by STIC: 12/8/05

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IFW16

## RAW SEQUENCE LISTING

DATE: 12/08/2005

PATENT APPLICATION: US/10/725,188A

TIME: 09:42:48

Input Set : A:\US 10\_725188 Seq Listing ST25.txt  
 Output Set: N:\CRF4\12082005\J725188A.raw

3 <110> APPLICANT: National University of Singapore  
 4       Sin, Yoke Min  
 5       Teh, Hsiao Chuin  
 6       Lim, Sze Yun  
 8 <120> TITLE OF INVENTION: Oral Vaccine, Method for its Preparation and Use Thereof  
 10 <130> FILE REFERENCE: 2500-000017  
 12 <140> CURRENT APPLICATION NUMBER: US 10/725,188A  
 13 <141> CURRENT FILING DATE: 2003-12-01  
 15 <160> NUMBER OF SEQ ID NOS: 9  
 17 <170> SOFTWARE: PatentIn version 3.3  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1810  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Aeromonas hydrophila  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: 5'UTR  
 27 <222> LOCATION: (1)..(480)  
 29 <220> FEATURE:  
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 31 <222> LOCATION: (481)..(1599)  
 33 <220> FEATURE:  
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 48 aaatcgatgg gcccgcggcc gctctagaag tactctcgag aagcttttg aattctttgg       120  
 50 atcctcggcg tggccatgg cctgttcggc gggttcgctc tgccagcggt tggggccgag       180  
 52 gtgatccgac ctcttcttct atttataagg cgagtcgtcg ttattgtgtg ataaatcacc       240  
 54 aattcggacg aattttgcca gcggttatcg ctgtaaacgt tttccatgg cgtgcaaaca       300  
 56 atgtgggatt caggtcacaa ttttccgct gtgactatgc ttttcgtaaa aagtccaaag       360  
 58 tttttcatt gcggatttggaa aaacccgggtg ctagtcgtcg cgccatagtg atgcaaagta       420  
 60 catcgctaac acaggaaata acaacgactt agtgttaat tacagtaggc attggaaact       480  
 62 atg aaa aag aca att ctg gct att gct atc ccg gct ctg ttt gca tcc       528  
 63 Met Lys Lys Thr Ile Leu Ala Ile Ala Ile Pro Ala Leu Phe Ala Ser  
 64 -20                   -15                   -10                   -5  
 66 gcc gct aac gct gca gtg gtt tac gac aaa gac ggt acc act ttt gac       576  
 67 Ala Ala Asn Ala Ala Val Val Tyr Asp Lys Asp Gly Thr Thr Phe Asp

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71	Val	Tyr	Gly	Arg	Val	Gln	Ala	Asn	Tyr	Tyr	Gly	Asp	His	Asn	Lys	Ser	
72	15								20					25			
74	gta	gct	acc	gat	ggt	tcc	tgg	ggc	ttc	agc	gga	act	ggt	acc	ccg	672	
75	Val	Ala	Ala	Thr	Asp	Gly	Ser	Trp	Gly	Phe	Ser	Gly	Thr	Gly	Thr	Pro	
76	30								35				40				
78	gaa	tat	act	cct	ggt	acc	gct	gct	cat	tac	tct	gat	ggt	gat	gag	720	
79	Glu	Tyr	Thr	Pro	Gly	Thr	Ala	Ala	His	Tyr	Ser	Asp	Val	Asp	Gly	Glu	
80	45								50			55		60			
82	ctg	gtt	ggt	tct	tcc	cgt	ctg	ggt	tgg	tcc	ggt	aag	att	gcc	ctg	816	
83	Leu	Val	Gly	Ser	Ser	Arg	Leu	Gly	Trp	Ser	Gly	Lys	Ile	Ala	Leu	Asn	
84									65			70		75			
86	aac	acc	tgg	tcc	ggt	atc	gcc	aag	act	gag	tgg	caa	gtt	tct	gct	864	
87	Asn	Thr	Trp	Ser	Gly	Ile	Ala	Lys	Thr	Glu	Trp	Gln	Val	Ser	Ala	Glu	
88									80			85		90			
90	aac	tcc	gcc	aac	aag	ttc	gat	tcc	cgt	cac	atc	tac	gtt	ggt	ttc	912	
91	Asn	Ser	Ala	Asn	Lys	Phe	Asp	Ser	Arg	His	Ile	Tyr	Val	Gly	Phe	Asp	
92									95			100		105			
94	ggc	acc	cag	tac	ggt	aag	atc	atc	ttc	ggt	cag	acc	gat	acc	gcg	912	
95	Gly	Thr	Gln	Tyr	Gly	Lys	Ile	Ile	Phe	Gly	Gln	Thr	Asp	Thr	Ala	Phe	
96									110			115		120			
98	tat	gac	gtg	ctg	gaa	ccg	acc	gat	atc	ttc	aac	gag	tgg	ggc	gac	960	
99	Tyr	Asp	Val	Leu	Glu	Pro	Thr	Asp	Ile	Phe	Asn	Glu	Trp	Gly	Asp	Val	
100	125								130			135		140			
102	ggt	aac	ttc	tat	gac	ggt	cgt	caa	gaa	ggt	cag	atc	atc	tac	tcc	1008	
103	Gly	Asn	Phe	Tyr	Asp	Gly	Arg	Gln	Glu	Gly	Gln	Ile	Ile	Tyr	Ser	Asn	
104									145			150		155			
106	acc	tac	ggt	ggc	ttc	aaa	ggc	aaa	ctg	tcc	tat	caa	acc	aac	gac	1056	
107	Thr	Tyr	Gly	Gly	Phe	Lys	Gly	Lys	Leu	Ser	Tyr	Gln	Thr	Asn	Asp	Asp	
108									160			165		170			
110	aag	gcc	gtc	aag	gtt	act	gac	gta	ggt	cag	ggc	atc	aaa	gaa	aac	gca	1104
111	Lys	Ala	Val	Lys	Val	Thr	Asp	Val	Gly	Gln	Gly	Ile	Lys	Glu	Asn	Ala	
112									175			180		185			
114	gtg	tac	ggc	aag	gat	gtt	aag	cgt	aac	tac	ggt	tat	gcc	gcg	gct	1152	
115	Val	Tyr	Gly	Lys	Asp	Val	Lys	Arg	Asn	Tyr	Gly	Tyr	Ala	Ala	Ala		
116									190			195		200			
118	ggt	tat	gac	ttc	gac	ttc	ggt	ctg	aac	gca	ggt	tac	tcc	tac		1200	
119	Gly	Tyr	Asp	Phe	Asp	Phe	Gly	Leu	Gly	Leu	Asn	Ala	Gly	Tyr	Ser	Tyr	
120	205								210			215		220			
122	tcc	gat	ctg	gaa	aat	acc	gca	acc	aac	act	ggc	gac	aag	aaa	gag	1248	
123	Ser	Asp	Leu	Glu	Asn	Thr	Ala	Thr	Asn	Asn	Thr	Gly	Asp	Lys	Glu		
124									225			230		235			
126	tgg	gca	ctg	ggt	gca	cac	tac	gcc	atc	aac	ggt	ttc	tac	ttc	gcc	1296	
127	Trp	Ala	Leu	Gly	Ala	His	Tyr	Ala	Ile	Asn	Gly	Phe	Tyr	Phe	Ala	Gly	
128									240			245		250			
130	gtc	tac	acc	cag	gca	gat	ctg	agc	tat	gac	acc	acc	acc	ggt	ggt	gac	1344
131	Val	Tyr	Thr	Gln	Ala	Asp	Leu	Ser	Tyr	Asp	Thr	Thr	Gly	Gly	Asp		
132									255			260		265			

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134 aag gac aag ggc cgt ggc tac gag ctg gct gct tcc tac aac gtt gat	1392
135 Lys Asp Lys Gly Arg Gly Tyr Glu Leu Ala Ala Ser Tyr Asn Val Asp	
136 270 275 280	
138 gcc tgg act ttc ctg gcc ggc tac aac ttc act gaa ggt aaa gtt gct	1440
139 Ala Trp Thr Phe Leu Ala Gly Tyr Asn Phe Thr Glu Gly Lys Val Ala	
140 285 290 295 300	
142 tcc aac acc gct ggt gct gag tac aaa gac atc gtt gac gaa acc ctg	1488
143 Ser Asn Thr Ala Gly Ala Glu Tyr Lys Asp Ile Val Asp Glu Thr Leu	
144 305 310 315	
146 ctg ggc gta cag tac gct ttc act tcc aag ctg aaa gcc tac acc gag	1536
147 Leu Gly Val Gln Tyr Ala Phe Thr Ser Lys Leu Lys Ala Tyr Thr Glu	
148 320 325 330	
150 tac aag atc cag ggt atc gac aag atg gac gac gag tgg acc gtt gcc	1584
151 Tyr Lys Ile Gln Gly Ile Asp Lys Met Asp Asp Glu Trp Thr Val Ala	
152 335 340 345	
154 ctg caa tac aac ttc taatctagcc tctgcgttga ttttagatgat gaacggccaa	1639
155 Leu Gln Tyr Asn Phe	
156 350	
158 gcttgcttgg ccgtttgtt ttatctgctt cccacctgat gtttctgttc tcttctgttg	1699
160 attatcttct ccttgcgcctc tttgacttgc gtcagttcac gttgtcttt ttctgtactt	1759
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167 <212> TYPE: PRT	
168 <213> ORGANISM: Aeromonas hydrophila	
170 <400> SEQUENCE: 2	
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177 -1 1 5 10	
180 Val Tyr Gly Arg Val Gln Ala Asn Tyr Tyr Gly Asp His Asn Lys Ser	
181 15 20 25	
184 Val Ala Ala Thr Asp Gly Ser Trp Gly Phe Ser Gly Thr Gly Thr Pro	
185 30 35 40	
188 Glu Tyr Thr Pro Gly Thr Ala Ala His Tyr Ser Asp Val Asp Gly Glu	
189 45 50 55 60	
192 Leu Val Gly Ser Ser Arg Leu Gly Trp Ser Gly Lys Ile Ala Leu Asn	
193 65 70 75	
196 Asn Thr Trp Ser Gly Ile Ala Lys Thr Glu Trp Gln Val Ser Ala Glu	
197 80 85 90	
200 Asn Ser Ala Asn Lys Phe Asp Ser Arg His Ile Tyr Val Gly Phe Asp	
201 95 100 105	
204 Gly Thr Gln Tyr Gly Lys Ile Ile Phe Gly Gln Thr Asp Thr Ala Phe	
205 110 115 120	
208 Tyr Asp Val Leu Glu Pro Thr Asp Ile Phe Asn Glu Trp Gly Asp Val	
209 125 130 135 140	
212 Gly Asn Phe Tyr Asp Gly Arg Gln Glu Gly Gln Ile Ile Tyr Ser Asn	
213 145 150 155	
216 Thr Tyr Gly Gly Phe Lys Lys Leu Ser Tyr Gln Thr Asn Asp Asp	

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221	175	180	185	
224	Val Tyr Gly Lys Asp Val Lys Arg Asn Tyr Gly	Tyr Ala Ala Ala Ala		
225	190	195	200	
228	Gly Tyr Asp Phe Asp Phe Gly Leu Gly Leu	Asn Ala Gly Tyr Ser Tyr		
229	205	210	215	220
232	Ser Asp Leu Glu Asn Thr Ala Thr Asn Asn	Thr Gly Asp Lys Lys Glu		
233	225	230	235	
236	Trp Ala Leu Gly Ala His Tyr Ala Ile Asn Gly	Phe Tyr Phe Ala Gly		
237	240	245	250	
240	Val Tyr Thr Gln Ala Asp Leu Ser Tyr Asp Thr	Thr Thr Gly Gly Asp		
241	255	260	265	
244	Lys Asp Lys Gly Arg Gly Tyr Glu Leu Ala Ala	Ser Tyr Asn Val Asp		
245	270	275	280	
248	Ala Trp Thr Phe Leu Ala Gly Tyr Asn Phe	Thr Glu Gly Lys Val Ala		
249	285	290	295	300
252	Ser Asn Thr Ala Gly Ala Glu Tyr Lys Asp	Ile Val Asp Glu Thr Leu		
253	305	310	315	
256	Leu Gly Val Gln Tyr Ala Phe Thr Ser Lys	Leu Lys Ala Tyr Thr Glu		
257	320	325	330	
260	Tyr Lys Ile Gln Gly Ile Asp Lys Met Asp Asp	Glu Trp Thr Val Ala		
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264	Leu Gln Tyr Asn Phe			
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271	<213> ORGANISM: Aeromonas hydrophila			
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283	<221> NAME/KEY: mat_peptide			
284	<222> LOCATION: (61)..(1119)			
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288	Met Lys Lys Thr Ile Leu Ala Ile Ala Ile Pro Ala Leu Phe Ala Ser			
289	-20	-15	-10	-5
291	gcc gct aac gct gca gtg gtt tac gac aaa gac ggt acc act ttt gac		96	
292	Ala Ala Asn Ala Ala Val Val Tyr Asp Lys Asp Gly Thr Thr Phe Asp			
293	-1 1	5	10	
295	gta tac ggc cgt gtt cag gct aac tac tac ggt gac cac aac aaa tct		144	
296	Val Tyr Gly Arg Val Gln Ala Asn Tyr Tyr Gly Asp His Asn Lys Ser			
297	15	20	25	
299	gta gct gct acc acc gat ggt tcc tgg ggc ttc agc gga act ggt acc ccg		192	

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304	Glu	Tyr	Thr	Pro	Gly	Thr	Ala	Ala	His	Tyr	Ser	Asp	Val	Asp	Gly	Glu	
305	45															60	
307	ctg	gtt	ggt	tct	tcc	cgt	ctg	ggt	tgg	tcc	ggt	aag	att	gcc	ctg	aac	288
308	Leu	Val	Gly	Ser	Ser	Arg	Leu	Gly	Trp	Ser	Gly	Lys	Ile	Ala	Leu	Asn	
309																75	
311	65															336	
312	Asn	Thr	Trp	Ser	Gly	Ile	Ala	Lys	Thr	Glu	Trp	Gln	Val	Ser	Ala	Glu	
313		80														90	
315	aac	tcc	gcc	aac	aag	ttc	gat	tcc	cgt	cac	atc	tac	gtt	ggt	ttc	gac	384
316	Asn	Ser	Ala	Asn	Lys	Phe	Asp	Ser	Arg	His	Ile	Tyr	Val	Gly	Phe	Asp	
317		95														105	
319	ggc	acc	cag	tac	ggt	aag	atc	atc	ttc	ggt	cag	acc	gat	acc	gcg	ttc	432
320	Gly	Thr	Gln	Tyr	Gly	Lys	Ile	Ile	Phe	Gly	Gln	Thr	Asp	Thr	Ala	Phe	
321		110														120	
323	tat	gac	gtg	ctg	gaa	ccg	acc	gat	atc	ttc	aac	gag	tgg	ggc	gac	gta	480
324	Tyr	Asp	Val	Leu	Glu	Pro	Thr	Asp	Ile	Phe	Asn	Glu	Trp	Gly	Asp	Val	
325		125														140	
327	ggt	aac	ttc	tat	gac	ggt	cgt	caa	gaa	ggt	cag	atc	atc	tac	tcc	aac	528
328	Gly	Asn	Phe	Tyr	Asp	Gly	Arg	Gln	Glu	Gly	Gln	Ile	Ile	Tyr	Ser	Asn	
329																155	
331	acc	tac	ggt	ggc	ttc	aaa	ggc	aaa	ctg	tcc	tat	caa	acc	aac	gac	gac	576
332	Thr	Tyr	Gly	Gly	Phe	Lys	Gly	Lys	Leu	Ser	Tyr	Gln	Thr	Asn	Asp	Asp	
333		160														170	
335	aag	gcc	gtc	aag	gtt	act	gac	gta	ggt	cag	ggc	atc	aaa	gaa	aac	gca	624
336	Lys	Ala	Val	Lys	Val	Thr	Asp	Val	Gly	Gln	Gly	Ile	Lys	Glu	Asn	Ala	
337		175														185	
339	gtg	tac	ggc	aag	gat	gtt	aag	cgt	aac	tac	ggt	tat	gcc	gcg	gct	gcc	672
340	Val	Tyr	Gly	Lys	Asp	Val	Lys	Arg	Asn	Tyr	Gly	Tyr	Ala	Ala	Ala	Ala	
341		190														200	
343	ggt	tat	gac	ttc	gac	ttc	ggt	ctg	ggt	ctg	aac	gca	ggt	tac	tcc	tac	720
344	Gly	Tyr	Asp	Phe	Asp	Phe	Gly	Leu	Gly	Leu	Asn	Ala	Gly	Tyr	Ser	Tyr	
345		205														220	
347	tcc	gat	ctg	gaa	aat	acc	gca	acc	aac	act	ggc	gac	aag	aaa	gag	768	
348	Ser	Asp	Leu	Glu	Asn	Thr	Ala	Thr	Asn	Asn	Thr	Gly	Asp	Lys	Lys	Glu	
349																235	
351	tgg	gca	ctg	ggt	gca	cac	tac	gcc	atc	aac	ggt	ttc	tac	ttc	gcc	ggt	816
352	Trp	Ala	Leu	Gly	Ala	His	Tyr	Ala	Ile	Asn	Gly	Phe	Tyr	Phe	Ala	Gly	
353		240														250	
355	gtc	tac	acc	cag	gca	gat	ctg	agc	tat	gac	acc	acc	ggt	ggt	gac	864	
356	Val	Tyr	Thr	Gln	Ala	Asp	Leu	Ser	Tyr	Asp	Thr	Thr	Gly	Gly	Asp		
357		255														265	
359	aag	gac	aag	ggc	cgt	ggc	tac	gag	ctg	gct	tcc	tac	aac	gtt	gat	912	
360	Lys	Asp	Lys	Gly	Arg	Gly	Tyr	Glu	Leu	Ala	Ala	Ser	Tyr	Asn	Val	Asp	
361		270														280	
363	gcc	tgg	act	ttc	ctg	gcc	ggc	tac	aac	ttc	act	gaa	ggt	aaa	gtt	gct	960
364	Ala	Trp	Thr	Phe	Leu	Ala	Gly	Tyr	Asn	Phe	Thr	Glu	Gly	Lys	Val	Ala	

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